Fscn2 Cas9-CKO Strategy

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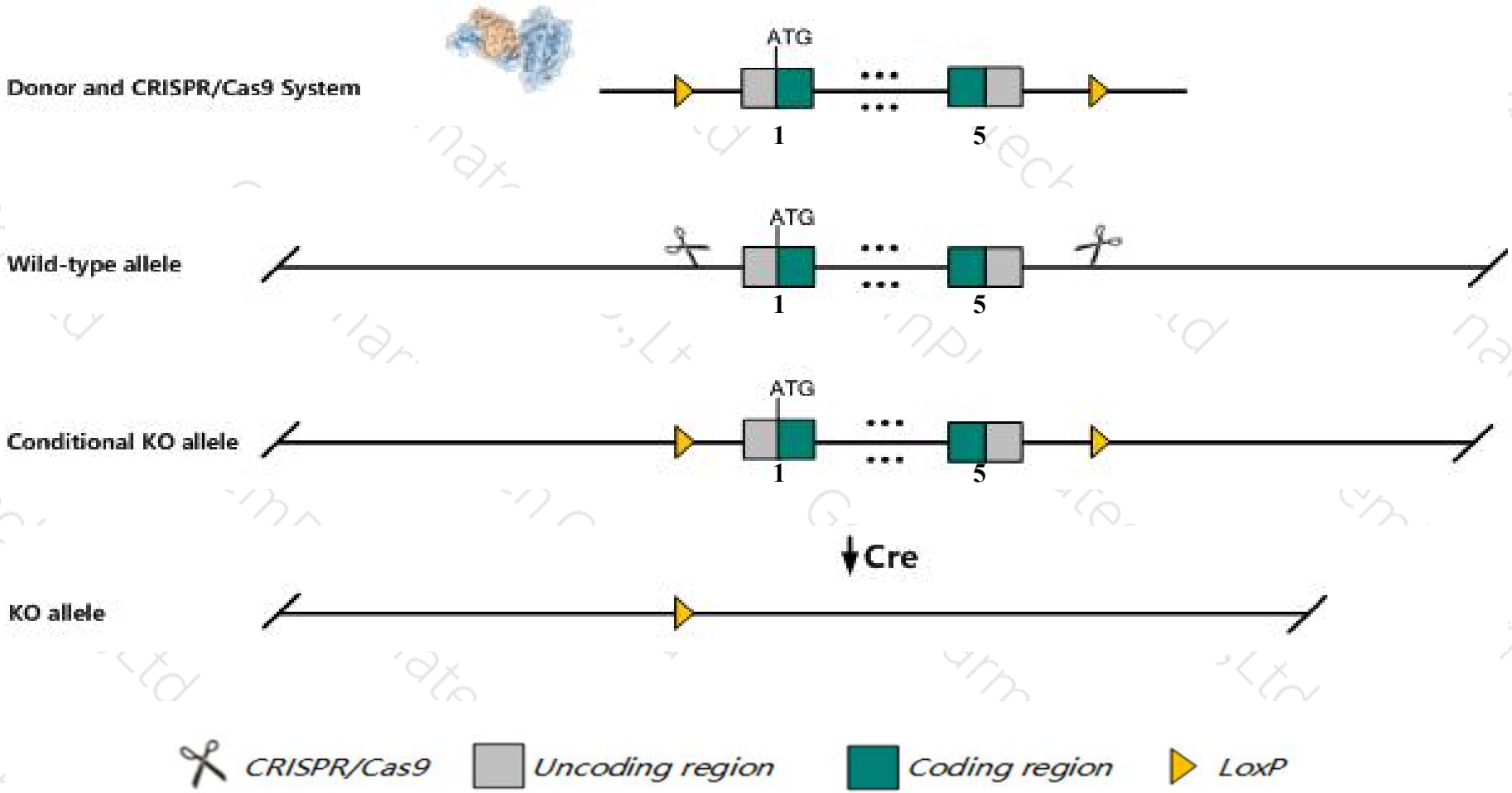
Project Overview

Project Name	***Fscn2***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fscn2* gene. The schematic diagram is as follows:



Technical routes

- The *Fscn2* gene has 3 transcripts. According to the structure of *Fscn2* gene, exon1-exon5 of *Fscn2-201* (ENSMUST00000026445.2) transcript is recommended as the knockout region.The region contains all of the coding sequence.Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Fscn2* gene. The brief process is as follows:CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice.Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Notice

- According to the existing MGI data,Mice homozygous for disruptions in this gene display retinal generation with structural abnormalities of the outer segment and depressed rod and cone ERGs that worsen with age.
- The floxed region is near to the C-terminal of *Faap100* gene,this strategy may influence the regulatory function of the C-terminal of *Faap100* gene.
- The *Fscn2* gene is located on the Chr11. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.
- This Strategy is designed based on genetic information in existing databases.Due to the complexity of biological processes, all risk of loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

集萃药康 GemPharmatech

Fscn2 fascin actin-bundling protein 2 [*Mus musculus* (house mouse)]

Gene ID: 238021, updated on 3-Feb-2020

Summary

Official Symbol	Fscn2 provided by MGI
Official Full Name	fascin actin-bundling protein 2 provided by MGI
Primary source	MGI:MGI:2443337
See related	Ensembl:ENSMUSG00000025380
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Ahl8; A930022G03; C630046B20Rik
Expression	Low expression observed in reference dataset See more
Orthologs	human all

Genomic context

Location: 11; 11 E2

See Fscn2 in Genome Data Viewer

Exon count: 5

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	11	NC_000077.6 (120360165..120368173)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	11	NC_000077.5 (120222848..120229487)

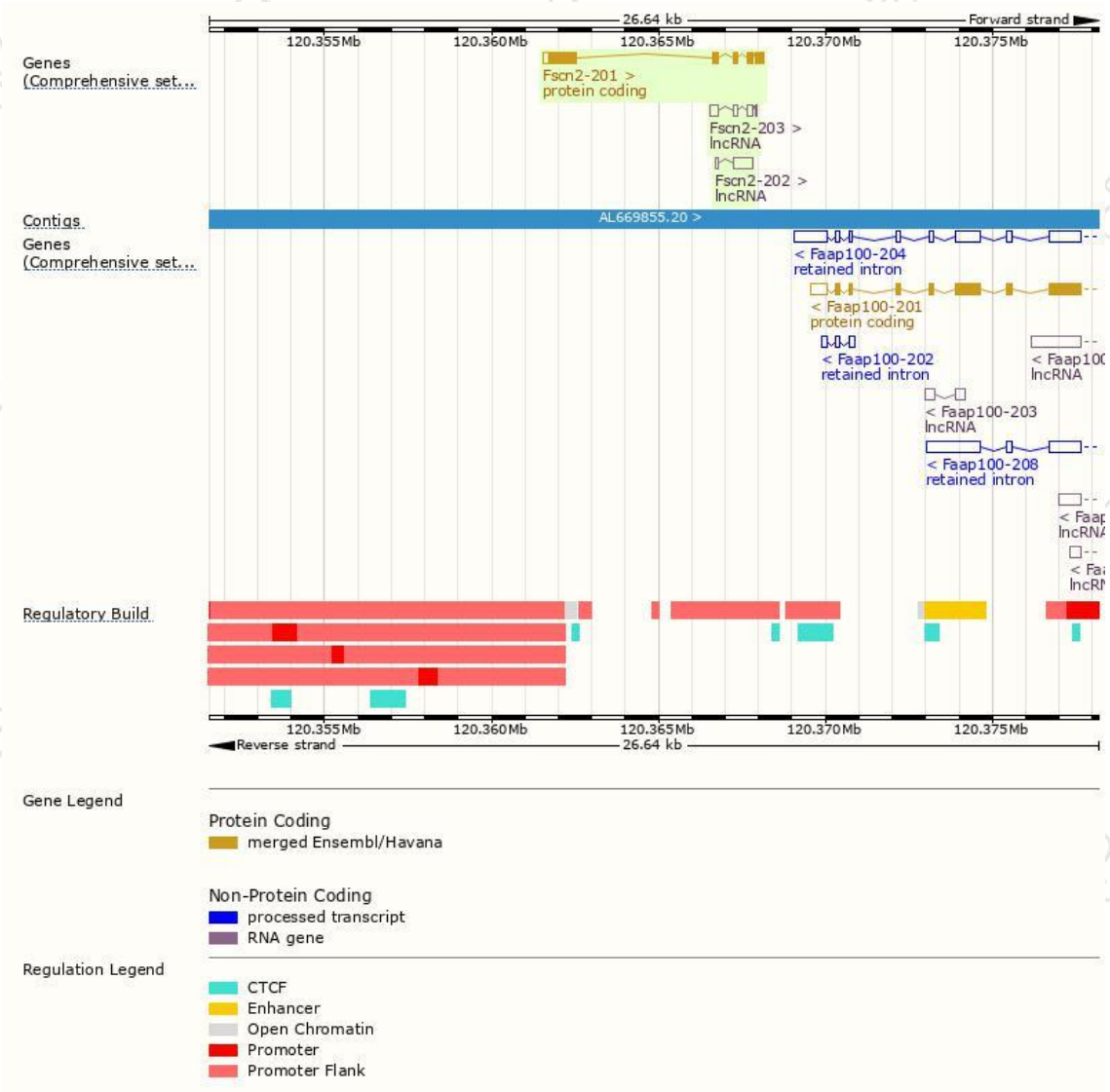
Transcript information（Ensembl）

The gene has 3 transcripts,all transcripts are shown below:

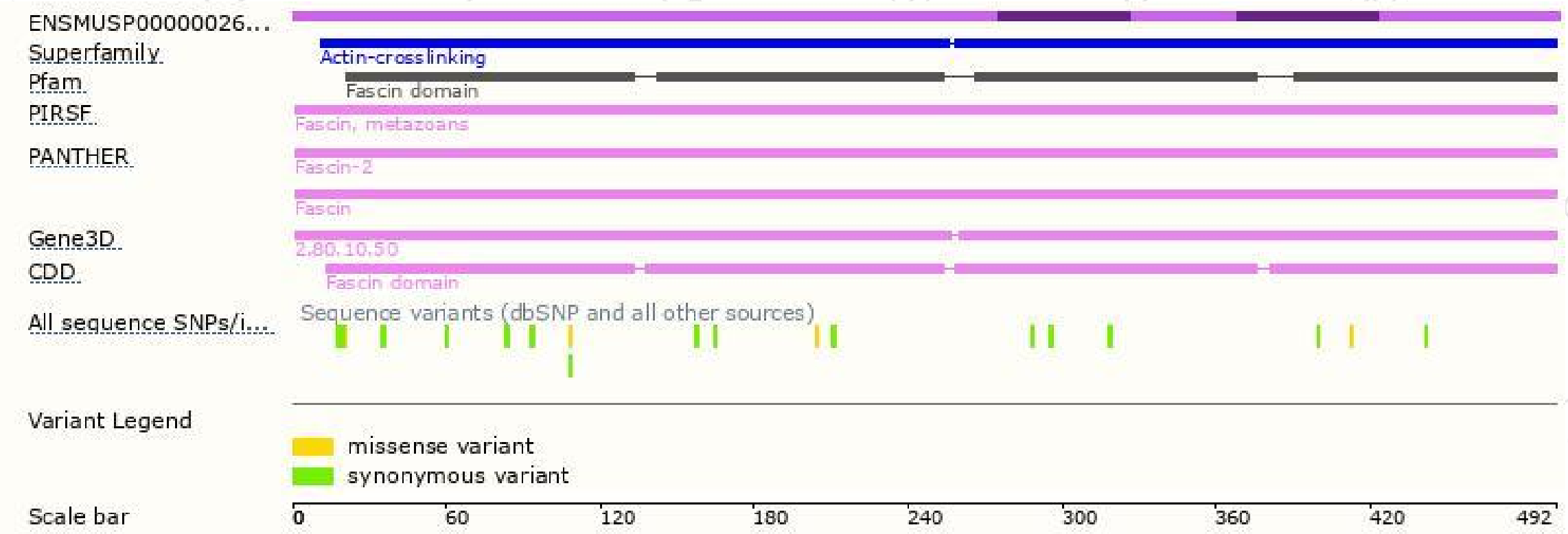
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fscn2-201	ENSMUST00000026445.2	1713	492aa	Protein coding	CCDS25731	Q32M02	TSL:1 GENCODE basic APPRIS P1
Fscn2-202	ENSMUST00000130476.1	669	No protein	lncRNA	-	-	TSL:3
Fscn2-203	ENSMUST00000152556.1	591	No protein	lncRNA	-	-	TSL:2

The strategy is based on the design of *Fscn2-201* transcript,The transcription is shown below

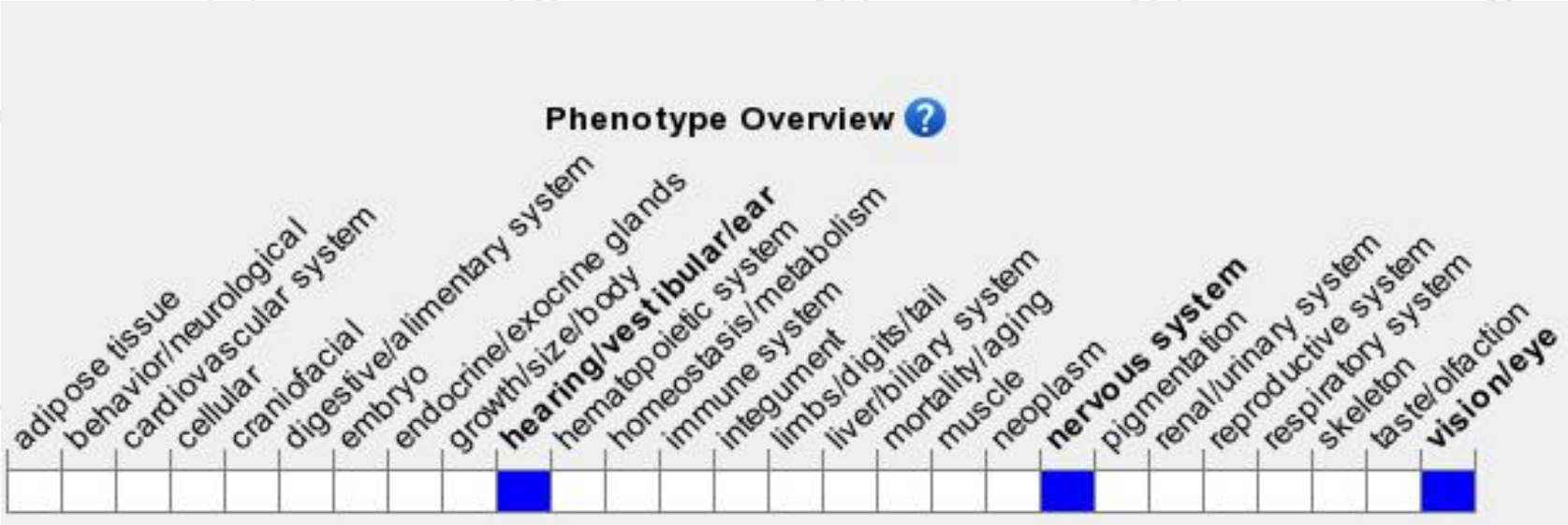
Genomic location distribution



Protein domain



Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

According to the existing MGI data,Mice homozygous for disruptions in this gene display retinal generation with structural abnormalities of the outer segment and depressed rod and cone ERGs that worsen with age.

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If you have any questions, you are welcome to inquire.

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